

BLASTP ALIGNMENT OF SEQ ID NO: 4 METALLOCARBOXYPEPTIDASE-LIKE POLYPEPTIDE WITH BOTHROPS JARARACA CARBOXYPEPTIDASE HOMOLOG SEQ ID NO: 20

Query: Metallocarboxypeptidase-like protein (SEQ ID 4)
Subject: >gb|AAF01344.1| (AF190274) carboxypeptidase homolog [Bothrops jararaca] (SEQ ID NO: 20)
Length = 416

Score = 826 (295.8 bits), Expect = 3.2e-82, P = 3.2e-82
Identities = 152/.326 (46%), Positives = 219/326 (67%)

Query: 13 MIVPGGLGYDRSLAQRQEIIVDKSVSPWSLET-YSYNIYHPMGEIYEWMMREISEKYKEW 71
+L GL Y+ L + Q ++D+ + + Y+Y Y+ +I W +I+ + +V
Sbjct: 82 ILQSGSLNVE-ILIDNLQAVLDRQLDNHARTAGYNEYKYSWEKIDAWTADIANENPSLV 140

Query: 72 TQHFGLGVTYETHPIYLYKISQPSGNPKKIIMDCGIHAREWIAPAFQWVKEILQNHKD 131
++ +G T+E P+ LK+ +P N KK I++DCG HAREWI+PAFCQWV+E ++ +
Sbjct: 141 SRLQIGTTFEGRPMPLLKVGKPGVN-KKAIFIDCGFHAREWISPAFCQWVREAVRTY GK 199

Query: 132 NSRIRKLLRNLDYFVLPVLNIDGYIYTWTTDRLWRKSRSPHNNGTCFGTDLNRNFNASWC 191
+ + +LL LDFY+LPVLNIDGY+Y+W R+WRK+RS + TC GTD NRNF+A+WC
Sbjct: 200 ETIMTQLLNKLDFYILPVLNIDGYVYSWKQSRMWRKTRSVNAGSTCIGTDPNRRNFDAAWC 259

Query: 192 SIGASRNCQDQTFCGTGPVSEPETKAVASFIESKKDDILCFLTMHSYGQLILTPYGYTKN 251
S+GASRN +T+CG+ P SE ETKA+A FI + I +LT+HSY Q++L PY YT +
Sbjct: 260 SVGASRNPCTSETYCGSKPESEKETKALADFIRNRRIIQAYLTIHSYSQMLLYPYSYTYD 319

Query: 252 KSSNHPMIQVGQKAANALKAKYGTNYRVGSSADILYASSGSSRDWARDIGIPFSYTFEL 311
+SN+ ++ + ++A LK +GT Y G A +Y ++G S DWA D GI +++TFEL
Sbjct: 320 LTSNNKKLNSIAKEAIRELKVLFGEITYGPGAAITYPAGGSDWAYDQGIKYAFTFEL 379

Query: 312 RDSGTGFLVLPDAQIPTCEETMEAV 337
RD G YGF LPE+QI+PTCEETM AV
Sbjct: 380 RDKGRYGFALPESQIKPTCEETMI AV 405

FIG: 1

BLASTP ALIGNMENT OF SEQ ID NO: 4 METALLOCARBOXYPEPTIDASE-LIKE POLYPEPTIDE WITH HUMAN CARBOXYPEPTIDASE B MUTANT (G251N, D253R)-HCPB-(HIS)6-C-MYC SEQ ID NO: 21

Query: Carboxypeptidase-like protein (SEQ ID 4)
 Subject: >sp|W13751|W13751 Carboxypeptidase B mutant (G251N,D253R)-HCPB-(His)6-c-myc (SEQ ID NO: 21)
 Length = 349

Score = 811 (290.5 bits), Expect = 6.2e-81, P = 6.2e-81
 Identities = 150/312 (48%), Positives = 206/312 (66%)

Query:	45	YSNYIHPMGEIYEMRMREISEKYKEVVTQHFLGVTYETHPIYYLKI	SPSGNPKKIWM	104
Sbjct:		+SY Y+ I W ++++ + +++++ +G T+E IY LK+ + +G K I+MD		
Query:	26	HSYEKYNKWETIEAWTQQVATENPALISRSVIGTTFEGRAIYLLKV	GK-AGQNKPAIFMD	84
Query:	105	CGIHAREWIAPAFQWVFVKEILQNHKDNSRIRKLLRNLDYFVLPVL	NIDGIYTWTDRL	164
Sbjct:		CG HAREWI+PAFCQWV+E ++ + +LL LDFVLPVLNIDGIYTW	R	
Query:	85	CGFHAREWISPAFCQWVFVREAVRTYGREIQVTELLDKLDFVLPVL	NIDGIYTWTKSRF	144
Query:	165	WRKSRSPHNNGTCTGTDLNRNFNASWCSIGASRNCQDQTFCTGTP	VPSEPETKAVASFIES	224
Sbjct:		WRK+RS H +C GTD NRNF+A WC IGASRN D+T+CG SE ETKA+A FI +		
Query:	145	WRKTRSTHTGSSCIGTDPNRNFDAGWCEIGASRNPCEITYCGPAAE	SEKETKALADFIRN	204
Query:	225	KKDDILCFLTMHSYQQLILTPYGYTKNKSNNHPEMIQVQKAANAL	KAKYGTNYRVGSSA	284
Sbjct:		K I +LT+HSY Q+++ PY Y N+ E+ + + L + +GT Y G A		
Query:	205	KLSSIKAYLTIHSYSQMMIYPYSYAYKLGENNAELNALAKATVKEL	ASLHGTYGPGA	264
Query:	285	DILYASSGSSRDWARDIGIPFSYTFELRDSGTYGFVLP	PEAQIQPTCEETMEA---VLS-V	340
Sbjct:		+Y ++G+SRDWA D GI +S+TFELRD+G YGF+LPE+QI+ TCEET A V S V		
Query:	265	TTIYPAGNSRDWAYDQGIYSFTFELRDTGRYGFLLPESQIRATCEET	FLAIKYVASV	324
Query:	341	LDDVYAKHWHSD	352	
Sbjct:		L+ +Y H H +		
Query:	325	LEHLYHHHHHHE	336	